peptides of said panel being the same length, wherein, in each library, said fixed position is (a) at least five residues from both ends of the peptides or (b) within the middle 50% of the peptides,

wherein the amino acid is assigned to said fixed position is not the same in all libraries of said panel,

each library being a separate and physically distinct entity from all other libraries of the panel,

in which the peptides are displayed on viruses.

30 (twice amended). A structured panel consisting of a plurality of biased combinatorial linear peptide libraries, each library having one and only one constant residue at a position fixed for all peptides in all libraries of said panel, all peptides of said panel being the same length, wherein, in each library, said fixed position is (a) at least five residues from both ends of the peptides or (b) within the middle 50% of the peptides,

wherein the amino acid is assigned to said fixed position is not the same in all libraries of said panel,

each library being a separate and physically distinct entity from all other libraries of the panel in which the peptides are displayed on viruses

wherein said peptides are of the form

$(Xaa)_m-R1-(Xaa)_n$,

where R1 is the amino acid at said first fixed position, and m and n do not differ by more than two,

in which R1 is tryptophan, proline or tyrosine.

32 (amended). A structured panel of biased combinatorial linear peptide libraries, each library comprising a plurality of different peptides, all peptides of said panel being the same length, each library having exactly two constant residue positions, one at a first position and the other at a second position,

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where the first position is fixed for all libraries in the panel, and is assigned the same residue for all peptides in any given library, but libraries of the panel collectively present a plurality of different residues at said first position,

where said first position is (a) at least five amino acids from both ends of the peptides, or (b) is in the middle 50% of the peptides,

where said panel comprises a plurality of subpanels, each comprising a plurality of libraries, and in each subpanel, the location of the second position is constant, but said location varies from subpanel to subpanel so the second positions of said subpanels, collectively scan all residue positions except for said first position,

where the second position is assigned the same residue for all peptides in a given library but the libraries of a given subpanel collectively present a plurality of different residues at said second position,

where one or more of the other positions of said libraries are variable positions, at which a given library exhibits a plurality of different residues as a result of sequence variation from peptide to peptide,

each library being a separate and physically distinct entity from the other libraries of the panel.

33 (amended). A structured panel of biased combinatorial linear peptide libraries, each library comprising a plurality of different peptides, all peptides of said panel being the same length, each library having exactly two biased residue positions, one at a first position and the other at a second position, the amino acids allowed in each library at said biased positions being only a subset of the set of amino acids allowed at the remaining positions of said library, and also being only a subset of the set of amino acids allowed at that biased position in the panel as a whole,

where the first position is fixed for all libraries in the panel,

where said first position is (a) at least five amino acids from both ends of the peptides, or (b) is in the middle 50% of the peptides,

where said panel comprises a plurality of subpanels, each comprising a plurality of libraries, and in each subpanel, the location of the second position is constant, but said location varies from subpanel to subpanel so the second positions of said subpanels collectively scan all residue positions except for said first position,

each library being a separate and physically distinct entity from the other libraries of the panel.

35 (amended). A structured panel of biased combinatorial linear peptide libraries, each library comprising a plurality of different peptides, all peptides of said panel being the same length, each library having exactly two biased residue positions, one at a first position and the other at a second position, the amino acids allowed in each library at said biased positions being only a subset of the set amino acids allowed at the remaining positions of said library, and also being only a subset of the set of amino acids allowed at that biased position in the panel as a whole,

where the first position is fixed for all libraries in the panel,

where said first position is (a) at least five amino acids from both ends of the peptides, or (b) is in the middle 50% of the peptides,

where each library is obtained by mixing a plurality of different mixed oligonucleotides, each oligonucleotide comprising one fully variable codon and one less variable codon, the position of the less variable codon varying so that said plurality collectively scan also positions other than said first

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